

Kaushal

1633

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/155,327A

DATE: 03/07/2000
TIME: 13:27:41

Input Set: I155327A.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

Does Not Comply
Corrected Diskette Needed

1 <110> APPLICANT: AMRAD Operations Pty Ltd
2 <120> TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
3 FAMILY OF APOPTOSIS-CONTROLLING GENES
4 <130> FILE REFERENCE: 2096584
5 <140> CURRENT APPLICATION NUMBER: US/09/155,327A
6 <141> CURRENT FILING DATE: 1999-03-29
7 <150> EARLIER APPLICATION NUMBER: PN8965
8 <151> EARLIER FILING DATE: 1996-03-27
9 <160> NUMBER OF SEQ ID NOS: 9
10 <170> SOFTWARE: PatentIn Ver. 2.1
11 <210> SEQ ID NO 1
12 <211> LENGTH: 33
13 <212> TYPE: DNA
14 <213> ORGANISM: Mouse
15 <220> FEATURE:
16 <221> NAME/KEY: modified_base
17 <222> LOCATION: 16
18 <223> OTHER INFORMATION: r is inosine
19 <220> FEATURE:
20 <221> NAME/KEY: modified_base
21 <222> LOCATION: 19
22 <223> OTHER INFORMATION: r is inosine
23 <220> FEATURE:
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25 <222> LOCATION: 22
26 <223> OTHER INFORMATION: r is inosine
27 <220> FEATURE:
28 <221> NAME/KEY: modified_base
29 <222> LOCATION: 25
30 <223> OTHER INFORMATION: r is inosine
31 <400> SEQUENCE: 1
32 gctctagaac tgggggrrrrr ttrtrgcctt ytt
33 <210> SEQ ID NO 2
34 <211> LENGTH: 9
35 <212> TYPE: PRT
36 <213> ORGANISM: Mouse
37 <220> FEATURE:
38 <221> NAME/KEY: Unsure
39 <222> LOCATION: 5
40 <223> OTHER INFORMATION: Xaa is Ile or Val
41 <400> SEQUENCE: 2
42 Asn Trp Gly Arg Xaa Val Ala Phe Phe
43 1 5
44 <210> SEQ ID NO 3

pg 1-2

invalid - per sequence
Rubs, r can only
represent a or g; instead,
use n and explain in
<220> - <223> section

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MAR 20 2000
TC 1600 MAIL ROOM

w--> OK

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RAW SEQUENCE LISTING
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TIME: 13:27:41

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47 <213> ORGANISM: Mouse
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49 <221> NAME/KEY: modified_base
50 <222> LOCATION: 14
51 <223> OTHER INFORMATION: r is inosine
52 <220> FEATURE:
53 <221> NAME/KEY: modified_base
54 <222> LOCATION: 17
55 <223> OTHER INFORMATION: r is inosine
56 <220> FEATURE:
57 <221> NAME/KEY: modified_base
58 <222> LOCATION: 20
59 <223> OTHER INFORMATION: r is inosine
60 <400> SEQUENCE: 3
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63 <211> LENGTH: 8
64 <212> TYPE: PRT
65 <213> ORGANISM: Mouse
66 <220> FEATURE:
67 <221> NAME/KEY: Unsure
68 <222> LOCATION: 4
69 <223> OTHER INFORMATION: Xaa is Asp or Glu
70 <220> FEATURE:
71 <221> NAME/KEY: Unsure
72 <222> LOCATION: 5
73 <223> OTHER INFORMATION: Xaa is Asn or Gln
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76 1 5
77 <210> SEQ ID NO 5
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80 <213> ORGANISM: Mouse
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82 Met Ala Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val
83 1 5 10
84 <210> SEQ ID NO 6
85 <211> LENGTH: 583
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87 <213> ORGANISM: HUMAN
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89 <221> NAME/KEY: CDS
90 <222> LOCATION: (1)..(579)
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93 Met Ala Thr Pro Ala Ser Ala Pro Asp Thr Arg Ala Leu Val Ala Asp
94 1 5 10 15

same error

31

w-->OK

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RAW SEQUENCE LISTING
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95      ttt gta ggt tat aag ctg agg cag aag ggt tat gtc tgt gga gct ggc      96
96      Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
97              20              25              30
98      ccc ggg gag ggc cca gca gct gac ccg ctg cac caa gcc atg cgg gca      144
99      Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
100              35              40              45
101      gct gga gat gag ttc gag acc cgc ttc cgg cgc acc ttc tct gat ctg      192
102      Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
103              50              55              60
104      gcg gct cag ctg cat gtg acc cca ggc tca gcc cag caa cgc ttc acc      240
105      Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
106              65              70              75              80
107      cag gtc tcc gac gaa ctt ttt caa ggg ggc ccc aac tgg ggc cgc ctt      288
108      Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
109              85              90              95
110      gta gcc ttc ttt ctc ttt ggg gct gca ctg tgt gct gag agt gtc aac      336
111      Val Ala Phe Phe Leu Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
112              100              105              110
113      aag gag atg gaa cca ctg gtg gga caa gtg cag gag tgg atg gtg gcc      384
114      Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala
115              115              120              125
116      tac ctg gag acg cgg ctg gtc gac tgg atc cac agc agt ggg ggc tgg      432
117      Tyr Leu Glu Thr Arg Leu Val Asp Trp Ile His Ser Ser Gly Gly Trp
118              130              135              140
119      gcg gag ttc aca gct cta tac ggg gac ggg gcc ctg gag gag gcg cgg      480
120      Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg
121      145              150              155              160
122      cgt ctg cgg gag ggg aac tgg gca tca gtg agg aca gtg ctg acg ggg      528
123      Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
124              165              170              175
125      gcc gtg gca ctg ggg gcc ctg gta act gta ggg gcc ttt ttt gct agc      576
126      Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
127              180              185              190
128      aag tgaa      583
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130      <210> SEQ ID NO 7
131      <211> LENGTH: 193
132      <212> TYPE: PRT
133      <213> ORGANISM: HUMAN
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139      Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
140              35              40              45
141      Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
142              50              55              60
143      Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
144              65              70              75              80

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145      Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
146                      85                      90                      95
147      Val Ala Phe Phe Leu Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
148                      100                      105                      110
149      Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala
150                      115                      120                      125
151      Tyr Leu Glu Thr Arg Leu Val Asp Trp Ile His Ser Ser Gly Gly Trp
152                      130                      135                      140
153      Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg
154      145                      150                      155                      160
155      Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
156                      165                      170                      175
157      Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
158                      180                      185                      190
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161      <211> LENGTH: 581
162      <212> TYPE: DNA
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166      <222> LOCATION: (1)..(579)
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170      1                      5                      10                      15
171      ttt gta ggc tat agg ctg agg cag aag ggt tat gtc tgt gga gct ggg      96
172      Phe Val Gly Tyr Arg Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
173      20                      25                      30
174      cct ggg gaa ggc cca gcc gcc gac ccg ctg cac caa gcc atg cgg gct      144
175      Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
176      35                      40                      45
177      gct gga gac gag ttt gag acc cgt ttc cgc cgc acc ttc tct gac ctg      192
178      Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
179      50                      55                      60
180      gcc gct cag cta cac gtg acc cca ggc tca gcc cag caa cgc ttc acc      240
181      Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
182      65                      70                      75                      80
183      cag gtt tcc gac gaa ctt ttc caa ggg ggc cct aac tgg ggc cgt ctt      288
184      Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
185      85                      90                      95
186      gtg gca ttc ttt gtc ttt ggg gct gcc ctg tgt gct gag agt gtc aac      336
187      Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
188      100                      105                      110
189      aaa gaa atg gag cct ttg gtg gga caa gtc cag gat tgg atc gtg gcc      384
190      Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Ile Val Ala
191      115                      120                      125
192      tac ctg gag aca cgt ctg gct gac tgg atc cac agc agt ggc ggc tgg      432
193      Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
194      130                      135                      140

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/155,327A

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195      gcg gac ttc aca gct cta tac ggg gac ggg gcc ctg gag gac gca cgg      480
196      Ala Asp Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Asp Ala Arg
197      145                      150                      155                      160
198      cgt ctg cgg gag ggc aac tgg gca tga gtg agc aca gtg gtg acg ggg      528
199      Arg Leu Arg Glu Gly Asn Trp Ala Val Ser Thr Val Val Thr Gly Ala
200                      165                      170                      175
201      gcc gtg gca ctg ggg gcc ctg gta act gta ggg gcc ttt ttt gct agc      576
202      Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser Lys
203                      180                      185                      190
204      aag tg      581
205      <210> SEQ ID NO 9
206      <211> LENGTH: 192
207      <212> TYPE: PRT
208      <213> ORGANISM: Mouse
209      <400> SEQUENCE: 9
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212      Phe Val Gly Tyr Arg Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
213                      20                      25                      30
214      Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
215      35                      40                      45
216      Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
217      50                      55                      60
218      Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
219      65                      70                      75                      80
220      Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
221                      85                      90                      95
222      Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
223      100                      105                      110
224      Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Ile Val Ala
225      115                      120                      125
226      Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
227      130                      135                      140
228      Ala Asp Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Asp Ala Arg
229      145                      150                      155                      160
230      Arg Leu Arg Glu Gly Asn Trp Ala Val Ser Thr Val Val Thr Gly
231                      165                      170                      175
232      Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
233                      180                      185                      190
234      Lys

```

Input Set: I155327A.RAW

Line ? Error/Warning

Original Text

42 W "N" or "Xaa" used: Feature required
75 W "N" or "Xaa" used: Feature required

Asn Trp Gly Arg Xaa Val Ala Phe Phe
Trp Ile Gln Xaa Xaa Gly Gly Trp